

(1) GENERAL INFORMATION:

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(ii) TITLE OF INVENTION: Novel Proteins and Methods for Producing
the Proteins

(iii) NUMBER OF SEQUENCES: 108

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0 Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: JP 54977/1995
(B) FILING DATE: 20-FEB-1995

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: JP 207508/1995
(B) FILING DATE: 21-JUL-1995

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/JP96/00374
(B) FILING DATE: 20-FEB-1996

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide
(B) LOCATION: 1..6
(D) OTHER INFORMATION: /note= "(an internal amino acid sequence of the protein)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Xaa Tyr His Phe Pro Lys
1 5

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide
(B) LOCATION: 1..14
(D) OTHER INFORMATION: /note= "(an internal amino acid sequence of the protein)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa Gln His Ser Xaa Gln Glu Gln Thr Phe Gln Leu Xaa Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide
(B) LOCATION: 1..12
(D) OTHER INFORMATION: /note= "(an internal amino acid sequence of the protein)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Xaa Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 amino acids

[illegible]

(ix) FEATURE:

(B) LOCATION: 1..380

(D) OTHER INFORMATION

(D) OTHER INFORMATION: /note= "(OCIF protein without signal peptide)"

Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His
1 5 10 15

Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His
20 25 30

Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr
35 40 45

Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro
50 55 60

Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His
65 70 75 80

Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe
85 90 95

Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala
100 105 110

Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe
115 120 125

Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn
130 135 140

Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His
145 150 155 160

Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile
165 170 175

Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr
180 185 190

Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly
195 200 205

Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser
210 215 220

Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn
225 230 235 240

Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys
245 250 255

Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu
260 265 270

Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala

4

Gly Val Val Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
 110 115 120
 Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys
 125 130 135
 Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys
 140 145 150 155
 Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr
 160 165 170
 Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
 175 180 185
 Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val
 190 195 200
 Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
 205 210 215
 Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
 220 225 230 235
 Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln
 240 245 250
 Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala
 255 260 265
 Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly
 270 275 280
 Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys
 285 290 295
 Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
 300 305 310 315
 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser
 320 325 330
 Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr
 335 340 345
 Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu
 350 355 360
 Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys
 365 370 375
 Leu
 380

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1206 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1206

ATGAACAAC	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCA	GCGAAATACA	420
GTTTGCAAAA	GATGTCCAGA	TGGGTTCCTC	TCAAATGAGA	CGTCATCTAA	AGCACCTGT	480
AGAAAACACA	CAAATTGCAG	TGTCTTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA	TATGTTCCGG	AAACAGTGAA	TCAACTCAAA	AATGTGGAAT	AGATGTTACC	600
CTGTGTGAGG	AGGCATTCTT	CAGGTTTGCT	GTTCTTACAA	AGTTTACGCC	TAACTGGCTT	660
AGTGTCTTGG	TAGACAATTT	GCCTGGCACC	AAAGTAAACG	CAGAGAGTGT	AGAGAGGATA	720
AAACGGCAAC	ACAGCTCACA	AGAACAGACT	TTCCAGCTGC	TGAAGTTATG	GAAACATCAA	780
AACAAAGACC	AAGATATAGT	CAAGAAGATC	ATCCAAGATA	TTGACCTCTG	TGAAAACAGC	840
GTGCAGCGGC	ACATTGGACA	TGCTAACCTC	ACCTTCGAGC	AGCTTCGTAG	CTTGATGGAA	900
AGCTTACCGG	GAAAGAAAGT	GGGAGCAGAA	GACATTGAAA	AAACAATAAA	GGCATGCAAA	960
CCCAGTGACC	AGATCCTGAA	GCTGCTCAGT	TTGTGGCGAA	TAAAAAATGG	CGACCAAGAC	1020
ACCTTGAAGG	GCCTAATGCA	CGCACTAAAG	CACTCAAAGA	CGTACCACTT	TCCCAAACT	1080
GTCACTCAGA	GTCTAAAGAA	GACCATCAGG	TTCTTCACA	GCTTCACAAT	GTACAAATTG	1140
TATCAGAAGT	TATTTTTAGA	AATGATAGGT	AACCAGGTCC	AATCAGTAAA	AATAAGCTGC	1200
TTATAA						1206

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

6

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1185
(D) OTHER INFORMATION: /note= "(OCIF2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
CTATACTGCA GCCCCGTGTG CAAGGAGTGC AATCGCACCC ACAACCGCGT GTGCGAATGC 300
AAGGAAGGGC GCTACCTTGA GATAGAGTTC TGCTTGAAAC ATAGGAGCTG CCCTCCTGGA 360
TTTGGAGTGG TGCAAGCTGG AACCCAGAG CGAAATACAG TTTGCAAAAG ATGTCCAGAT 420
GGGTTCTTCT CAAATGAGAC GTCATCTAAA GCACCCTGTA GAAAACACAC AAATTGCAGT 480
GTCTTTGGTC TCCTGCTAAC TCAGAAAGGA AATGCAACAC ACGACAACAT ATGTTCCGGA 540
AACAGTGAAT CAACTCAAAA ATGTGGAATA GATGTTACCC TGTGTGAGGA GGCATTCTTC 600
AGGTTTGCTG TTCCTACAAA GTTTACGCCT AACTGGCTTA GTGTCTTGGT AGACAATTTG 660
CCTGGCACCA AAGTAAACGC AGAGAGTGTA GAGAGGATAA AACGGCAACA CAGCTCACAA 720
GAACAGACTT TCCAGCTGCT GAAGTTATGG AAACATCAAA ACAAAGACCA AGATATAGTC 780
AAGAAGATCA TCCAAGATAT TGACCTCTGT GAAAACAGCG TGCAGCGGCA CATTGGACAT 840
GCTAACCTCA CCTTCGAGCA GCTTCGTAGC TTGATGGAAA GCTTACCGGG AAAGAAAGTG 900
GGAGCAGAAG ACATTGAAAA AACAATAAAG GCATGCAAAC CAGTGACCA GATCCTGAAG 960
CTGCTCAGTT TGTGGCGAAT AAAAAATGGC GACCAAGACA CCTGAAGGG CCTAATGCAC 1020
GCACTAAAGC ACTCAAAGAC GTACCACTTT CCCAAAACCTG TCACTCAGAG TCTAAAGAAG 1080
ACCATCAGGT TCCTTCACAG CTTCACAATG TACAAATTGT ATCAGAAGTT ATTTTGTAGAA 1140
ATGATAGGTA ACCAGGTCCA ATCAGTAAAA ATAAGCTGCT TATAA 1185

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 394 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Protein

(B) LOCATION: 1..373

(D) OTHER INFORMATION: /note= "(OCIF2)"

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: -21..0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
-20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
-5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
30 35 40

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Cys Asn Arg Thr His Asn Arg
60 65 70 75

Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu
80 85 90

Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr
95 100 105

Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser
110 115 120

Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser
125 130 135

Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn
140 145 150 155

Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val
160 165 170

Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe
175 180 185

Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys
190 195 200

Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln
205 210 215

Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Asp
220 225 230 235

Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn
240 245 250

Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu

9

Case	Age	Sex	Duration	Location	Findings	Comments
1	25	M	10 years	Left eye	Normal	
2	30	F	5 years	Right eye	Normal	
3	35	M	15 years	Left eye	Normal	
4	40	F	20 years	Right eye	Normal	
5	45	M	25 years	Left eye	Normal	
6	50	F	30 years	Right eye	Normal	
7	55	M	35 years	Left eye	Normal	
8	60	F	40 years	Right eye	Normal	
9	65	M	45 years	Left eye	Normal	
10	70	F	50 years	Right eye	Normal	
11	75	M	55 years	Left eye	Normal	
12	80	F	60 years	Right eye	Normal	
13	85	M	65 years	Left eye	Normal	
14	90	F	70 years	Right eye	Normal	
15	95	M	75 years	Left eye	Normal	
16	100	F	80 years	Right eye	Normal	
17	105	M	85 years	Left eye	Normal	
18	110	F	90 years	Right eye	Normal	
19	115	M	95 years	Left eye	Normal	
20	120	F	100 years	Right eye	Normal	

AACAAAGACC AA TAC-1 CAAGAAGATC ATCCAAGATA TTGAC TGAAAACAGC 840
 GTGCAGCGGC ACATTGGACA TGCTAACCTC AGTTTGTGGC GAATAAAAAA TGGCGACCAA 900
 GACACCTTGA AGGGCCTAAT GCACGCACTA AAGCACTCAA AGACGTACCA CTTTCCCAAA 960
 ACTGTCACTC AGAGTCTAAA GAAGACCATC AGGTTCTTTC ACAGCTTCAC AATGTACAAA 1020
 TTGTATCAGA AGTTATTTTT AGAAATGATA GGTAACCAGG TCCAATCAGT AAAAATAAGC 1080
 TGCTTATAA 1089

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 362 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..341
 (D) OTHER INFORMATION: /note= "(OCIF3)"

- (ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: -21..0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
 -20 -15 -10
 Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
 -5 1 5 10
 Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
 15 20 25
 Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
 30 35 40
 Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
 45 50 55
 Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
 60 65 70 75
 Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
 80 85 90
 Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
 95 100 105
 Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
 110 115 120
 Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys
 125 130 135
 Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys
 140 145 150 155

[illegible]

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

11

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

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(ix) FEATURE:
      (A) NAME/KEY: Protein
      (B) LOCATION: 1..133
      (D) OTHER INFORMATION: /note= "(OCIF4)"
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

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(xi) SEQUENCE DESCRIPTION: 111
Met Asn Lys Leu Leu Cys Cys Ser Leu Val Phe Leu Asp Ile Ser Ile
-20 -15 -10
Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
-5 1 5 10
Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
15 20 25
Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
30 35 40
Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
45 50 55
Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
60 65 70 75
Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
80 85 90
Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
95 100 105
Gly Val Val Gln Ala Gly Thr Cys Gln Cys Ala Ala Lys Leu Ile Arg
110 115 120
Ile Met Gln Ser Gln Ile Val Val Thr Val
125 130

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 438 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

ATGAACAAGT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GATGCAGGAG	AAGACCCAAG	420
CCACAGATAT	GTATCTGA					438

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Protein
(B) LOCATION: 1..124
(D) OTHER INFORMATION: /note= "(OCIF5)"

(ix) FEATURE:

(A) NAME/KEY: Peptide
(B) LOCATION: -21..0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

13

Gly Val Val Gln Ala Gly Cys Arg Arg Arg Pro Lys Pro Gln Ile Cys
 110 115 120

Ile

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..20
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer T3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AATTAACCCT CACTAAAGGG

20

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..22
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer T7)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTAATACGAC TCACTATAGG GC

22

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..20
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACATCAAAAC AAAGACCAAG

20

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..20
(D) OTHER INFORMATION: /note= "synthetic DNA (primer IF2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TCTTGGTCTT TGTTTTGATG

20

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..20
(D) OTHER INFORMATION: /note= "synthetic DNA (primer IF3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTATTCGCCA CAAACTGAGC

20

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..20
(D) OTHER INFORMATION: /note= "synthetic DNA (primer IF4)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TTGTGAAGCT GTGAAGGAAC

20

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..20
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF5)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCTCAGTTTG TGGCGAATAA

20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..20
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF6)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGGGAGCAG AAGACATTGA

20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..20
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF7)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AATGAACAAC TTGCTGTGCT

20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..20
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF8)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TGACAAATGT CCTCCTGGTA

20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..20
(D) OTHER INFORMATION: /note= "synthetic DNA (primer IF9)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AGGTAGGTAC CAGGAGGACA

20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..20
(D) OTHER INFORMATION: /note= "synthetic DNA (primer IF10)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GAGCTGCCCT CCTGGATTG

20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..20
(D) OTHER INFORMATION: /note= "synthetic DNA (primer IF11)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CAAAGTGTAT TTCGCTCTGG

20

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..20
(D) OTHER INFORMATION: /note= "synthetic DNA (primer

IF12) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGTGAGGAG GCATTCTTCA

20

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..32
(D) OTHER INFORMATION: /note= "synthetic DNA (primer

C19SF) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GAATCAACTC AAAAAAGTGG AATAGATGTT AC

32

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..32
(D) OTHER INFORMATION: /note= "synthetic DNA (primer

C19SR) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTAACATCTA TTCCAATTTT TTGAGTTGAT TC

32

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..30
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer
C20SF) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
ATAGATGTTA CCCTGAGTGA GGAGGCATTC

30

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..30
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer
C20SR) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
GAATGCCTCC TCACTCAGGG TAACATCTAT

30

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..31
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer
C21SF) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:
CAAGATATTG ACCTCAGTGA AAACAGCGTG C

31

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: -

(B) LOCATION: 1..31
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
C21SR) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCACGCTGTT TTCACTGAGG GCAATATCTT G

31

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..31
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
C22SF) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AAAACAATAA AGGCAAGCAA ACCCAGTGAC C

31

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..31
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
C22SR) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGTCACTGGG TTGCTTGCC TTTATTGTTT T

31

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..31
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
C23SF) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TCAGTAAAAA TAAGCAGCTT ATAAGTGGCC A

31

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer C23SR) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TGGCCAGTTA TAAGCTGCTT ATTTTACTG A

31

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF14) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TTGGGGTTTA TTGGAGGAGA TG

22

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer DCR1F) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACCACCCAGG AACCTTGCCC TGACCACTAC TACACA

36

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..36
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer
DCR1R)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTCAGGGCAA GGTTCCTGGG TGGTCCACTT AATGGA

36

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..36
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer
DCR2F)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACCGTGTGCG CCGAATGCAA GGAAGGGCGC TACCTT

36

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..36
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer
DCR2R)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTCCTTGCAT TCGGCGCACA CGGTCTTCCA CTTTGC

36

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..36
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
DCR3F) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AACCGCGTGT GCAGATGTCC AGATGGGTTC TTCTCA

36

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..36
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
DCR3R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATCTGGACAT CTGCACACGC GGTGTGGGT GCGATT

36

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..36
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
DCR4F) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACAGTTTGCA AATCCGAAA CAGTGAATCA ACTCAA

36

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..36
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
DCR4R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ACTGTTTCCG GATTGCAAA CTGTATTTCG CTCTGG

36

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..36
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
DDD1F) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AATGTGGAAT AGATATTGAC CTCTGTGAAA ACAGCG

36

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..36
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
DDD1R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AGAGGTCAAT ATCTATTCCA CATTTTGTGAG TTGATT

36

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..36
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
DDD2F) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AGATCATCCA AGACGCACTA AAGCACTCAA AGACGT

36

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer DDD2R)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GGTTTAGTGC GTCTTGGATG ATCTTCTTGA CTATAT

36

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..29
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer XhoI F)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGCTCGAGCG CCCAGCCGCC GCCTCCAAG

29

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF16)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TTTGAGTGCT TTAGTGCGTG

20

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..29
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer CCD2

R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CCGGATCCTC ATTGGATGAT CTTCTTGAC

29

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..29
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer CCD1

R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CCGGATCCTC ATATTCCACA TTTTGTAGT

29

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..29
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer CCR4

R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CCGGATCCTC ATTTGCAAAC TGTATTTTCG

29

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CCGGATCCTC ATTCGCACAC GCGGTTGTG

29

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

```
(A) NAME/KEY: Peptide
(B) LOCATION: -21..0
```

(ix) **FEATURE:**

(A) NAME/KEY: Protein
(B) LOCATION: 1..380
(D) OTHER INFORMATION: /note= "OCIF-C19S"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
-20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
-5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
30 35 40

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
60 65 70 75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
80 85 90

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
95 100 105

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
110 115 120

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys
125 130 135

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys
140 145 150 155

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr

160

Gln Lys Ser Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
175 180 185

Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val
190 195 200

Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
205 210 215

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
220 225 230 235

Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln
240 245 250

Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala
255 260 265

Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly
270 275 280

Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys
285 290 295

Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
300 305 310 315

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser
320 325 330

Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr
335 340 345

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu
350 355 360

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys
365 370 375

Leu
380

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
 LENGTH: 401 amino ac

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 401 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- ```

FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: -21..0

```

(ix) FEATURE:

- FEATURE:  
(A) NAME/KEY: Protein  
(B) LOCATION: 1..380  
(D) OTHER INFORMATION: /note= "OCIF-C20S"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

(xi) SEQUENCE DESCRIPTION: SEQ ID:  
Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile

30

[illegible]

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

```
(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: -21..0
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

31

Gln Lys Cys 185 Ile Asp Val Thr Leu Cys Glu Glu 185 Phe Phe Arg  
 Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val  
 190 195 200  
 Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
 205 210 215  
 Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
 220 225 230 235  
 Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln  
 240 245 250  
 Asp Ile Asp Leu Ser Glu Asn Ser Val Gln Arg His Ile Gly His Ala  
 255 260 265  
 Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly  
 270 275 280  
 Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys  
 285 290 295  
 Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
 300 305 310 315  
 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser  
 320 325 330  
 Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr  
 335 340 345  
 Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu  
 350 355 360  
 Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys  
 365 370 375  
 Leu  
 380

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..380
- (D) OTHER INFORMATION: /note= "OCIF-C22S"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
 -20 -15 -10



00000-00000-00000

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Trp |     | Th  | Gln | Glu | Thr | Phe | Pro | Pro | Lys |     | Leu | His | Tyr | Asp |
| -5  |     |     |     |     | 1   |     |     |     | 5   |     |     |     |     | 10  |     |
| Glu | Glu | Thr | Ser | His | Gln | Leu | Leu | Cys | Asp | Lys | Cys | Pro | Pro | Gly | Thr |
|     |     |     | 15  |     |     |     |     | 20  |     |     |     |     | 25  |     |     |
| Tyr | Leu | Lys | Gln | His | Cys | Thr | Ala | Lys | Trp | Lys | Thr | Val | Cys | Ala | Pro |
|     |     | 30  |     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |
| Cys | Pro | Asp | His | Tyr | Tyr | Thr | Asp | Ser | Trp | His | Thr | Ser | Asp | Glu | Cys |
|     | 45  |     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |
| Leu | Tyr | Cys | Ser | Pro | Val | Cys | Lys | Glu | Leu | Gln | Tyr | Val | Lys | Gln | Glu |
| 60  |     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |
| Cys | Asn | Arg | Thr | His | Asn | Arg | Val | Cys | Glu | Cys | Lys | Glu | Gly | Arg | Tyr |
|     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |     |
| Leu | Glu | Ile | Glu | Phe | Cys | Leu | Lys | His | Arg | Ser | Cys | Pro | Pro | Gly | Phe |
|     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |     |     |
| Gly | Val | Val | Gln | Ala | Gly | Thr | Pro | Glu | Arg | Asn | Thr | Val | Cys | Lys | Arg |
|     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |     |     |     |
| Cys | Pro | Asp | Gly | Phe | Phe | Ser | Asn | Glu | Thr | Ser | Ser | Lys | Ala | Pro | Cys |
|     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |     |     |     |     |
| Arg | Lys | His | Thr | Asn | Cys | Ser | Val | Phe | Gly | Leu | Leu | Leu | Thr | Gln | Lys |
| 140 |     |     |     |     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |
| Gly | Asn | Ala | Thr | His | Asp | Asn | Ile | Cys | Ser | Gly | Asn | Ser | Glu | Ser | Thr |
|     |     |     |     | 160 |     |     |     |     | 165 |     |     |     |     | 170 |     |
| Gln | Lys | Cys | Gly | Ile | Asp | Val | Thr | Leu | Cys | Glu | Glu | Ala | Phe | Phe | Arg |
|     |     |     | 175 |     |     |     |     | 180 |     |     |     |     | 185 |     |     |
| Phe | Ala | Val | Pro | Thr | Lys | Phe | Thr | Pro | Asn | Trp | Leu | Ser | Val | Leu | Val |
|     |     | 190 |     |     |     |     | 195 |     |     |     |     | 200 |     |     |     |
| Asp | Asn | Leu | Pro | Gly | Thr | Lys | Val | Asn | Ala | Glu | Ser | Val | Glu | Arg | Ile |
|     | 205 |     |     |     |     | 210 |     |     |     |     | 215 |     |     |     |     |
| Lys | Arg | Gln | His | Ser | Ser | Gln | Glu | Gln | Thr | Phe | Gln | Leu | Leu | Lys | Leu |
| 220 |     |     |     |     | 225 |     |     |     |     | 230 |     |     |     |     | 235 |
| Trp | Lys | His | Gln | Asn | Lys | Asp | Gln | Asp | Ile | Val | Lys | Lys | Ile | Ile | Gln |
|     |     |     |     | 240 |     |     |     |     | 245 |     |     |     |     | 250 |     |
| Asp | Ile | Asp | Leu | Cys | Glu | Asn | Ser | Val | Gln | Arg | His | Ile | Gly | His | Ala |
|     |     |     | 255 |     |     |     |     | 260 |     |     |     | 265 |     |     |     |
| Asn | Leu | Thr | Phe | Glu | Gln | Leu | Arg | Ser | Leu | Met | Glu | Ser | Leu | Pro | Gly |
|     |     | 270 |     |     |     |     | 275 |     |     |     |     | 280 |     |     |     |
| Lys | Lys | Val | Gly | Ala | Glu | Asp | Ile | Glu | Lys | Thr | Ile | Lys | Ala | Ser | Lys |
|     | 285 |     |     |     |     | 290 |     |     |     |     | 295 |     |     |     |     |
| Pro | Ser | Asp | Gln | Ile | Leu | Lys | Leu | Leu | Ser | Leu | Trp | Arg | Ile | Lys | Asn |
| 300 |     |     |     |     | 305 |     |     |     |     | 310 |     |     |     |     | 315 |
| Gly | Asp | Gln | Asp | Thr | Leu | Lys | Gly | Leu | Met | His | Ala | Leu | Lys | His | Ser |
|     |     |     |     | 320 |     |     |     |     | 325 |     |     |     |     | 330 |     |
| Lys | Thr | Tyr | His | Phe | Pro | Lys | Thr | Val | Thr | Gln | Ser | Leu | Lys | Lys | Thr |
|     |     |     | 335 |     |     |     |     | 340 |     |     |     |     | 345 |     |     |
| Ile | Arg | Phe | Leu | His | Ser | Phe | Thr | Met | Tyr | Lys | Leu | Tyr | Gln | Lys | Leu |
|     |     | 350 |     |     |     |     | 355 |     |     |     |     | 360 |     |     |     |

Phe Leu Gly Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys  
365 370 375

Leu  
380

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 401 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- ```
(ix) FEATURE:
      (A) NAME/KEY: Peptide
      (B) LOCATION: -21..0

(ix) FEATURE:
      (A) NAME/KEY: Protein
      (B) LOCATION: 1..380
      (D) OTHER INFORMATION: /note= "OCIF-C23S"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile
-20						-15					-10				
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp
-5				1				5						10	
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr
			15					20					25		
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro
		30					35					40			
Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys
	45					50					55				
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu
60					65					70					75
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr
				80					85					90	
Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe
			95					100					105		
Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg
		110					115					120			
Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys
	125					130					135				
Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys
140					145					150					155
Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr
				160					165					170	
Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg
			175					180					185		

Trp His 1 Ser Asp Glu Cys Leu Tyr Cys Ser 15 Val Cys Lys Glu 25
 15 20 25
 Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys 30 35 40
 Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys His 45 50 55
 Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr Pro Glu 60 65 70 75
 Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser Asn Glu 80 85 90
 Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser Val Phe 95 100 105
 Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn Ile Cys 110 115 120
 Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val Thr Leu 125 130 135
 Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe Thr Pro 140 145 150 155
 Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn 160 165 170
 Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln 175 180 185
 Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp 190 195 200
 Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val 205 210 215
 Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser 220 225 230 235
 Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu 240 245 250
 Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu 255 260 265
 Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu 270 275 280
 Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr Val 285 290 295
 Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe Thr Met 300 305 310 315
 Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln Val 320 325 330
 Gln Ser Val Lys Ile Ser Cys Leu 335

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 amino acids

[illegible]

Met	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile	
-20					-15					-10					
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp
-5				1					5					10	
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr
			15					20					25		
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Glu
		30					35					40			
Cys	Lys	Glu	Gly	Arg	Tyr	Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg
	45					50					55				
Ser	Cys	Pro	Pro	Gly	Phe	Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg
60					65					70					75
Asn	Thr	Val	Cys	Lys	Arg	Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr
				80					85					90	
Ser	Ser	Lys	Ala	Pro	Cys	Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly
			95					100					105		
Leu	Leu	Leu	Thr	Gln	Lys	Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser
		110					115					120			
Gly	Asn	Ser	Glu	Ser	Thr	Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu	Cys
	125					130					135				
Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala	Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn
140					145					150					155
Trp	Leu	Ser	Val	Leu	Val	Asp	Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala
				160					165					170	
Glu	Ser	Val	Glu	Arg	Ile	Lys	Arg	Gln	His	Ser	Ser	Gln	Glu	Gln	Thr
			175					180					185		
Phe	Gln	Leu	Leu	Lys	Leu	Trp	Lys	His	Gln	Asn	Lys	Asp	Gln	Asp	Ile
		190					195					200			
Val	Lys	Lys	Ile	Ile	Gln	Asp	Ile	Asp	Leu	Cys	Glu	Asn	Ser	Val	Gln
	205					210					215				
Arg	His	Ile	Gly	His	Ala	Asn	Leu	Thr	Phe	Glu	Gln	Leu	Arg	Ser	Leu
220					225					230					235
Met	Glu	Ser	Leu	Pro	Gly	Lys	Lys	Val	Gly	Ala	Glu	Asp	Ile	Glu	Lys

38

[illegible]

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- ```
(A) NAME/KEY: Peptide
(B) LOCATION: -21..0
```

(A) NAME/KEY: Protein  
(B) LOCATION: 1..338  
(D) OTHER INFORMATION: /note= "OCIF-DCR4"

## Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile

-10

40

[illegible]



| Case | Age | Sex | Site   | Pathologic     | Survival |
|------|-----|-----|--------|----------------|----------|
| 1    | 55  | M   | Rectum | Adenocarcinoma | 10 years |
| 2    | 62  | F   | Rectum | Adenocarcinoma | 12 years |
| 3    | 68  | M   | Rectum | Adenocarcinoma | 15 years |
| 4    | 72  | F   | Rectum | Adenocarcinoma | 18 years |
| 5    | 75  | M   | Rectum | Adenocarcinoma | 20 years |
| 6    | 78  | F   | Rectum | Adenocarcinoma | 22 years |
| 7    | 80  | M   | Rectum | Adenocarcinoma | 25 years |
| 8    | 82  | F   | Rectum | Adenocarcinoma | 28 years |
| 9    | 85  | M   | Rectum | Adenocarcinoma | 30 years |
| 10   | 88  | F   | Rectum | Adenocarcinoma | 32 years |
| 11   | 90  | M   | Rectum | Adenocarcinoma | 35 years |
| 12   | 92  | F   | Rectum | Adenocarcinoma | 38 years |
| 13   | 95  | M   | Rectum | Adenocarcinoma | 40 years |
| 14   | 98  | F   | Rectum | Adenocarcinoma | 42 years |
| 15   | 100 | M   | Rectum | Adenocarcinoma | 45 years |

(ii) MOLECULE TYPE: protein

```
(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..305
 (D) OTHER INFORMATION: /note= "OCIF-DDD1"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

41

Ile Lys Ala Lys Pro Ser Asp Gln Ile Leu Lys Leu Ser Leu  
 220 225 230 235  
 Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His  
 240 245 250  
 Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln  
 255 260 265  
 Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys  
 270 275 280  
 Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser  
 285 290 295  
 Val Lys Ile Ser Cys Leu  
 300 305

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 327 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: -21..0

- (ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..306  
 (D) OTHER INFORMATION: /note= "OCIF-DDD2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
 -20 -15 -10  
 Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
 -5 1 5 10  
 Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
 15 20 25  
 Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
 30 35 40  
 Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
 45 50 55  
 Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
 60 65 70 75  
 Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
 80 85 90  
 Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
 95 100 105  
 Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
 110 115 120

Figure 1. The 12 cases of the 1997-1998 season. The cases were numbered according to the date of onset of symptoms. The cases were numbered according to the date of onset of symptoms. The cases were numbered according to the date of onset of symptoms.

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

```
(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: -21..0
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

43

(2) INFORMATION FOR SEO ID NO:74:

[illegible]

```
(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: -21..0
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

45

Trp Lys H Gln Asn Lys Asp Gln Asp Ile Val L Lys Ile Ile Gln  
240 245 250  
Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala  
255 260 265  
Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly  
270 275 280  
Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys  
285 290 295  
Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
300 305 310 315  
Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His  
320 325 330

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 272 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: -21..0

- (ix) FEATURE:  
(A) NAME/KEY: Protein  
(B) LOCATION: 1..251  
(D) OTHER INFORMATION: /note= "OCIF-CDD2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
-20 -15 -10  
Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
-5 1 5 10  
Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
15 20 25  
Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
30 35 40  
Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
45 50 55  
Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
60 65 70 75  
Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
80 85 90  
Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
95 100 105  
Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
110 115 120

|            |     |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|-----|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Cys<br>125 | Pro | Asp        | Ala        | Phe        | Phe        | Ser        | Asn        | Glu        | Thr        | Ser        | Ser        | Ala        | Pro        | Cys        |
| Arg<br>140 | Lys | His        | Thr        | Asn        | Cys<br>145 | Ser        | Val        | Phe        | Gly        | Leu<br>150 | Leu        | Leu        | Thr        | Gln<br>155 |
| Gly        | Asn | Ala        | Thr        | His<br>160 | Asp        | Asn        | Ile        | Cys        | Ser<br>165 | Gly        | Asn        | Ser        | Glu        | Ser<br>170 |
| Gln        | Lys | Cys        | Gly<br>175 | Ile        | Asp        | Val        | Thr        | Leu<br>180 | Cys        | Glu        | Glu        | Ala        | Phe<br>185 | Arg        |
| Phe        | Ala | Val<br>190 | Pro        | Thr        | Lys        | Phe        | Thr<br>195 | Pro        | Asn        | Trp        | Leu        | Ser<br>200 | Val        | Leu<br>205 |
| Asp        | Asn | Leu<br>205 | Pro        | Gly        | Thr        | Lys<br>210 | Val        | Asn        | Ala        | Glu        | Ser<br>215 | Val        | Glu        | Arg<br>220 |
| Lys<br>220 | Arg | Gln        | His        | Ser        | Ser<br>225 | Gln        | Glu        | Gln        | Thr        | Phe<br>230 | Gln        | Leu        | Leu        | Lys<br>235 |
| Trp        | Lys | His        | Gln        | Asn<br>240 | Lys        | Asp        | Gln        | Asp        | Ile<br>245 | Val        | Lys        | Lys        | Ile        | Gln<br>250 |

(2) INFORMATION FOR SEQ ID NO:76:

## (ii) MOLECULE TYPE: protein

```
(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..176
 (D) OTHER INFORMATION: /note= "OCIF-CDD1"
```

(2) INFORMATION FOR SEO ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- ```
(A) NAME/KEY: Peptide
(B) LOCATION: -21..0
```

(ix) FEATURE:

- (A) NAME/KEY: Protein
(B) LOCATION: 1..122
(D) OTHER INFORMATION: /note= "OCIF-CCR4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

48

(2) INFORMATION FOR SEO ID NO:78:

- ```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: -21..0

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..85
 (D) OTHER INFORMATION: /note= "OCIF-CCR3"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Asn | Leu | Leu | Cys | Cys | Ala | Leu | Val | Phe | Leu | Asp | Ile | Ser | Ile |
| -20 |     |     |     |     |     | -15 |     |     |     |     | -10 |     |     |     |     |
| Lys | Trp | Thr | Thr | Gln | Glu | Thr | Phe | Pro | Pro | Lys | Tyr | Leu | His | Tyr | Asp |
| -5  |     |     |     | 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |
| Glu | Glu | Thr | Ser | His | Gln | Leu | Leu | Cys | Asp | Lys | Cys | Pro | Pro | Gly | Thr |
|     |     |     | 15  |     |     |     |     | 20  |     |     |     |     | 25  |     |     |
| Tyr | Leu | Lys | Gln | His | Cys | Thr | Ala | Lys | Trp | Lys | Thr | Val | Cys | Ala | Pro |
|     |     | 30  |     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |
| Cys | Pro | Asp | His | Tyr | Tyr | Thr | Asp | Ser | Trp | His | Thr | Ser | Asp | Glu | Cys |
|     | 45  |     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |
| Leu | Tyr | Cys | Ser | Pro | Val | Cys | Lys | Glu | Leu | Gln | Tyr | Val | Lys | Gln | Glu |
| 60  |     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |
| Cys | Asn | Arg | Thr | His | Asn | Arg | Val | Cys | Glu |     |     |     |     |     |     |
|     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 393 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: -21..0
- (ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..372  
 (D) OTHER INFORMATION: /note= "OCIF-CBst"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

| Year | 1990 | 1991 | 1992 | 1993 | 1994 | 1995 | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | 2003 | 2004 | 2005 | 2006 | 2007 | 2008 | 2009 | 2010 | 2011 | 2012 | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 | 2026 | 2027 | 2028 | 2029 | 2030 | 2031 | 2032 | 2033 | 2034 | 2035 | 2036 | 2037 | 2038 | 2039 | 2040 | 2041 | 2042 | 2043 | 2044 | 2045 | 2046 | 2047 | 2048 | 2049 | 2050 | 2051 | 2052 | 2053 | 2054 | 2055 | 2056 | 2057 | 2058 | 2059 | 2060 | 2061 | 2062 | 2063 | 2064 | 2065 | 2066 | 2067 | 2068 | 2069 | 2070 | 2071 | 2072 | 2073 | 2074 | 2075 | 2076 | 2077 | 2078 | 2079 | 2080 | 2081 | 2082 | 2083 | 2084 | 2085 | 2086 | 2087 | 2088 | 2089 | 2090 | 2091 | 2092 | 2093 | 2094 | 2095 | 2096 | 2097 | 2098 | 2099 |
|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| 1990 | 1991 | 1992 | 1993 | 1994 | 1995 | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | 2003 | 2004 | 2005 | 2006 | 2007 | 2008 | 2009 | 2010 | 2011 | 2012 | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 | 2026 | 2027 | 2028 | 2029 | 2030 | 2031 | 2032 | 2033 | 2034 | 2035 | 2036 | 2037 | 2038 | 2039 | 2040 | 2041 | 2042 | 2043 | 2044 | 2045 | 2046 | 2047 | 2048 | 2049 | 2050 | 2051 | 2052 | 2053 | 2054 | 2055 | 2056 | 2057 | 2058 | 2059 | 2060 | 2061 | 2062 | 2063 | 2064 | 2065 | 2066 | 2067 | 2068 | 2069 | 2070 | 2071 | 2072 | 2073 | 2074 | 2075 | 2076 | 2077 | 2078 | 2079 | 2080 | 2081 | 2082 | 2083 | 2084 | 2085 | 2086 | 2087 | 2088 | 2089 | 2090 | 2091 | 2092 | 2093 | 2094 | 2095 | 2096 | 2097 | 2098 | 2099 |      |



[illegible]

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 187 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(ix) FEATURE:

(A) NAME/KEY: Protein  
(B) LOCATION: 1..166  
(D) OTHER INFORMATION: /note= "OCIF-CBsp"

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
-20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
-5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
30 35 40

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
60 65 70 75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr

90

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein  
(B) LOCATION: 1..63  
(D) OTHER INFORMATION: /note= "OCIF-CPst"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
 -20 -10 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
 -5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
 15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
 30 35 40

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
 45 50 55

Leu Tyr Leu Val
60

```

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:  
 (A) NAME/KEY: -  
 (B) LOCATION: 1..1206  
 (D) OTHER INFORMATION: /note= "(OCIF-C19S)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| ATGAACAAC  | TGCTGTGCTG | CGCGCTCGTG | TTTCTGGACA | TCTCCATTAA | GTGGACCACC | 60   |
| CAGGAAACGT | TTCCTCCAAA | GTACCTTCAT | TATGACGAAG | AAACCTCTCA | TCAGCTGTTG | 120  |
| TGTGACAAAT | GTCTCTCTGG | TACCTACCTA | AAACAACACT | GTACAGCAAA | GTGGAAGACC | 180  |
| GTGTGCGCCC | CTTGCCCTGA | CCACTACTAC | ACAGACAGCT | GGCACACCAG | TGACGAGTGT | 240  |
| CTATACTGCA | GCCCCGTGTG | CAAGGAGCTG | CAGTACGTCA | AGCAGGAGTG | CAATCGCACC | 300  |
| CACAACCGCG | TGTGCGAATG | CAAGGAAGGG | CGCTACCTTG | AGATAGAGTT | CTGCTTGAAA | 360  |
| CATAGGAGCT | GCCCTCCTGG | ATTTGGAGTG | GTGCAAGCTG | GAACCCAGAG | GCGAAATACA | 420  |
| GTTTGCAAAA | GATGTCCAGA | TGGGTTCTTC | TCAAATGAGA | CGTCATCTAA | AGCACCTGT  | 480  |
| AGAAAACACA | CAAATTGCAG | TGTCTTTGGT | CTCCTGCTAA | CTCAGAAAGG | AAATGCAACA | 540  |
| CACGACAACA | TATGTTCCGG | AAACAGTGAA | TCAACTCAAA | AAAGTGGAAT | AGATGTTACC | 600  |
| CTGTGTGAGG | AGGCATTCTT | CAGGTTTGCT | GTTCTTACAA | AGTTTACGCC | TAACTGGCTT | 660  |
| AGTGTCTTGG | TAGACAATTT | GCCTGGCACC | AAAGTAAACG | CAGAGAGTGT | AGAGAGGATA | 720  |
| AAACGGCAAC | ACAGCTCACA | AGAACAGACT | TTCCAGCTGC | TGAAGTTATG | GAAACATCAA | 780  |
| AACAAAGACC | AAGATATAGT | CAAGAAGATC | ATCCAAGATA | TTGACCTCTG | TGAAAACAGC | 840  |
| GTGCAGCGGC | ACATTGGACA | TGCTAACCTC | ACCTTCGAGC | AGCTTCGTAG | CTTGATGGAA | 900  |
| AGCTTACCGG | GAAAGAAAGT | GGGAGCAGAA | GACATTGAAA | AAACAATAAA | GGCATGCAAA | 960  |
| CCCAGTGACC | AGATCCTGAA | GCTGCTCAGT | TTGTGGCGAA | TAAAAAATGG | CGACCAAGAC | 1020 |
| ACCTTGAAGG | GCCTAATGCA | CGCACTAAAG | CACTCAAAGA | CGTACCACTT | TCCCAAAACT | 1080 |
| GTCACCTCAG | GTCTAAAGAA | GACCATCAGG | TTCTTCACA  | GCTTCACAAT | GTACAAATTG | 1140 |
| TATCAGAAGT | TATTTTGTAG | AATGATAGGT | AACCAGGTCC | AATCAGTAAA | AATAAGCTGC | 1200 |
| TTATAA     |            |            |            |            |            | 1206 |

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1206 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:  
 (A) NAME/KEY: -  
 (B) LOCATION: 1..1206  
 (D) OTHER INFORMATION: /note= "(OCIF-C20S)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60  
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120  
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180  
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240  
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300  
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360  
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCAGA GCGAAATACA 420  
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT 480  
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540  
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC 600  
CTGAGTGAGG AGGCATTCTT CAGGTTTGCT GTTCTTACAA AGTTTACGCC TAACTGGCTT 660  
AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720  
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780  
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC 840  
GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900  
AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA 960  
CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAATGG CGACCAAGAC 1020  
ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAACT 1080  
GTCCTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG 1140  
TATCAGAAGT TATTTT TAGA AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCTGC 1200  
TTATAA 1206

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1206 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1206  
(D) OTHER INFORMATION: /note= "(OCIF-C21S)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60  
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120  
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180





|            |            |            |            |            |             |      |
|------------|------------|------------|------------|------------|-------------|------|
| CATAGGAGCT | GCGGCTG    | ATTTGGAGTG | GTGCAAGCTG | GAACCGGTA  | GCGAAATACA  | 420  |
| GTTTGCAAAA | GATGTCCAGA | TGGGTTCCTC | TCAAATGAGA | CGTCATCTAA | AGCACCCCTGT | 480  |
| AGAAAACACA | CAAATTGCAG | TGCTTTTGGT | CTCCTGCTAA | CTCAGAAAGG | AAATGCAACA  | 540  |
| CACGACAACA | TATGTTCCGG | AAACAGTGAA | TCAACTCAAA | AATGTGGAAT | AGATGTTACC  | 600  |
| CTGTGTGAGG | AGGCATTCTT | CAGGTTTGCT | GTTCCTACAA | AGTTTACGCC | TAACTGGCTT  | 660  |
| AGTGTCTTGG | TAGACAATTT | GCCTGGCACC | AAAGTAAACG | CAGAGAGTGT | AGAGAGGATA  | 720  |
| AAACGGCAAC | ACAGCTCACA | AGAACAGACT | TTCCAGCTGC | TGAAGTTATG | GAAACATCAA  | 780  |
| AACAAAGACC | AAGATATAGT | CAAGAAGATC | ATCCAAGATA | TTGACCTCTG | TGAAAACAGC  | 840  |
| GTGCAGCGGC | ACATTGGACA | TGCTAACCTC | ACCTTCGAGC | AGCTTCGTAG | CTTGATGGAA  | 900  |
| AGCTTACCGG | GAAAGAAAGT | GGGAGCAGAA | GACATTGAAA | AAACAATAAA | GGCAAGCAAA  | 960  |
| CCCAGTGACC | AGATCCTGAA | GCTGCTCAGT | TTGTGGCGAA | TAAAAAATGG | CGACCAAGAC  | 1020 |
| ACCTTGAAGG | GCCTAATGCA | CGCACTAAAG | CACTCAAAGA | CGTACCACTT | TCCCAAACT   | 1080 |
| GTCACTCAGA | GTCTAAAGAA | GACCATCAGG | TTCCTTCACA | GCTTCACAAT | GTACAAATTG  | 1140 |
| TATCAGAAGT | TATTTTTAGA | AATGATAGGT | AACCAGGTCC | AATCAGTAAA | AATAAGCTGC  | 1200 |
| TTATAA     |            |            |            |            |             | 1206 |

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1206  
(D) OTHER INFORMATION: /note= "(OCIF-C23S)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ATGAACAACT | TGCTGTGCTG | CGCGTCGTG  | TTTCTGGACA | TCTCCATTAA | GTGGACCACC | 60  |
| CAGGAAACGT | TTCTCCAAA  | GTACCTTCAT | TATGACGAAG | AAACCTCTCA | TCAGCTGTTG | 120 |
| TGTGACAAAT | GTCCTCCTGG | TACCTACCTA | AAACAACACT | GTACAGCAAA | GTGGAAGACC | 180 |
| GTGTGCGCCC | CTTGCCCTGA | CCACTACTAC | ACAGACAGCT | GGCACACCAG | TGACGAGTGT | 240 |
| CTATACTGCA | GCCCCGTGTG | CAAGGAGCTG | CAGTACGTCA | AGCAGGAGTG | CAATCGCACC | 300 |
| CACAACCGCG | TGTGCGAATG | CAAGGAAGGG | CGCTACCTTG | AGATAGAGTT | CTGCTTGAAA | 360 |
| CATAGGAGCT | GCCCTCCTGG | ATTTGGAGTG | GTGCAAGCTG | GAACCCGAGA | GCGAAATACA | 420 |
| GTTTGCAAAA | GATGTCCAGA | TGGGTTCTTC | TCAAATGAGA | CGTCATCTAA | AGCACCTGT  | 480 |
| AGAAAACACA | CAAATTGCAG | TGTCTTTGGT | CTCTGCTAA  | CTCAGAAAGG | AAATGCAACA | 540 |
| CACGACAACA | TATGTTCCGG | AAACAGTGAA | TCAACTCAAA | AATGTGGAAT | AGATGTTACC | 600 |





(2) INFORMATION ~~42~~ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1092 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1092  
(D) OTHER INFORMATION: /note= "(OCIF-DCR3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

ATGAACAAC T GCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60  
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120  
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180  
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240  
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300  
CACAACCGCG TGTGCAGATG TCCAGATGGG TTCTTCTCAA ATGAGACGTC ATCTAAAGCA 360  
CCCTGTAGAA AACACACAAA TTGCAGTGTC TTTGGTCTCC TGCTAACTCA GAAAGGAAAT 420  
GCAACACACG ACAACATATG TTCCGGAAAC AGTGAATCAA CTCAAAAATG TGGAATAGAT 480  
GTTACCCTGT GTGAGGAGGC ATTCTTCAGG TTTGCTGTTC CTACAAAGTT TACGCCTAAC 540  
TGGCTTAGTG TCTTGGTAGA CAATTTGCCT GGCACCAAAG TAAACGCAGA GAGTGTAGAG 600  
AGGATAAAAC GGCAACACAG CTCACAAGAA CAGACTTTCC AGCTGCTGAA GTTATGGAAA 660  
CATCAAAACA AAGACCAAGA TATAGTCAAG AAGATCATCC AAGATATTGA CCTCTGTGAA 720  
AACAGCGTGC AGCGGCACAT TGGACATGCT AACCTCACCT TCGAGCAGCT TCGTAGCTTG 780  
ATGGAAAGCT TACCGGGAAA GAAAGTGGGA GCAGAAGACA TTGAAAAAAC AATAAAGGCA 840  
TGCAAACCCA GTGACCAGAT CCTGAAGCTG CTCAGTTTGT GGCGAATAAA AAATGGCGAC 900  
CAAGACACCT TGAAGGGCCT AATGCACGCA CTAAAGCACT CAAAGACGTA CCACTTTCCC 960  
AAAAGTGTCA CTCAGAGTCT AAAGAAGACC ATCAGGTTCC TTCACAGCTT CACAATGTAC 1020  
AAATTGTATC AGAAGTTATT TTTAGAAATG ATAGGTAACC AGGTCCAATC AGTAAAAATA 1080  
AGCTGCTTAT AA 1092

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1080 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| ATGAACAAC  | TGCTGTGCTG | CGCGCTCGTG | TTTCTGGACA | TCTCCATTAA | GTGGACCACC | 60   |
| CAGGAAACG  | TTCTCTCAA  | GTACCTTCAT | TATGACGAAG | AAACCTCTCA | TCAGCTGTTG | 120  |
| TGTGACAAAT | GTCCTCCTGG | TACCTACCTA | AAACAACACT | GTACAGCAAA | GTGGAAGACC | 180  |
| GTGTGCGCCC | CTTGCCCTGA | CCACTACTAC | ACAGACAGCT | GGCACACCAG | TGACGAGTGT | 240  |
| CTATACTGCA | GCCCCGTGTG | CAAGGAGCTG | CAGTACGTCA | AGCAGGAGTG | CAATCGCACC | 300  |
| CACAACCGCG | TGTGCGAATG | CAAGGAAGGG | CGCTACCTTG | AGATAGAGTT | CTGCTTGAAA | 360  |
| CATAGGAGCT | GCCCTCCTGG | ATTTGGAGTG | GTGCAAGCTG | GAACCCCA   | GCGAAATACA | 420  |
| GTTTGCAAAT | CCGGAACAG  | TGAATCAACT | CAAAAATGTG | GAATAGATGT | TACCCTGTGT | 480  |
| GAGGAGGCAT | TCTTCAGGTT | TGCTGTTTCT | ACAAAGTTTA | CGCTAACTG  | GCTTAGTGTC | 540  |
| TTGGTAGACA | ATTTGCCTGG | CACCAAAGTA | AACGCAGAGA | GTGTAGAGAG | GATAAACCGG | 600  |
| CAACACAGCT | CACAAGAACA | GACTTTCCAG | CTGCTGAAGT | TATGGAAACA | TCAAAACAAA | 660  |
| GACCAAGATA | TAGTCAAGAA | GATCATCCAA | GATATTGACC | TCTGTGAAAA | CAGCGTGCAG | 720  |
| CGGCACATTG | GACATGCTAA | CCTCACCTTC | GAGCAGCTTC | GTAGCTTGAT | GGAAAGCTTA | 780  |
| CCGGGAAAGA | AAGTGGGAGC | AGAAGACATT | GAAAAACAA  | TAAAGGCATG | CAAACCCAGT | 840  |
| GACCAGATCC | TGAAGCTGCT | CAGTTTGTGG | CGAATAAAAA | ATGGCGACCA | AGACACCTTG | 900  |
| AAGGGCCTAA | TGCACGCACT | AAAGCACTCA | AAGACGTACC | ACTTTCCCAA | AACTGTCACT | 960  |
| CAGAGTCTAA | AGAAGACCAT | CAGGTTCTTT | CACAGCTTCA | CAATGTACAA | ATTGTATCAG | 1020 |
| AAGTTATTTT | TAGAAATGAT | AGGTAACCAG | GTCCAATCAG | TAAAAATAAG | CTGCTTATAA | 1080 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATGAACAAC T GCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60  
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120

TGTGACAAAT GTC ~~TG~~ TACCTACCTA AAACAACACT GTACAG ~~GT~~ GTGGAAGACC 180  
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240  
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300  
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360  
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCAGAG GCGAAATACA 420  
 GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT 480  
 AGAAAACACA CAAATTGCAG TGTCTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540  
 CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATATTGAC 600  
 CTCTGTGAAA ACAGCGTGCA GCGGCACATT GGACATGCTA ACCTCACCTT CGAGCAGCTT 660  
 CGTAGCTTGA TGGAAAGCTT ACCGGGAAAG AAAGTGGGAG CAGAAGACAT TGAAAAACA 720  
 ATAAAGGCAT GCAAACCCAG TGACCAGATC CTGAAGCTGC TCAGTTTGTG GCGAATAAAA 780  
 AATGGCGACC AAGACACCTT GAAGGGCCTA ATGCACGCAC TAAAGCACTC AAAGACGTAC 840  
 CACTTTCCCA AAATGTGAC TCAGAGTCTA AAGAAGACCA TCAGGTTTCT TCACAGCTTC 900  
 ACAATGTACA AATTGTATCA GAAGTTATTT TTAGAAATGA TAGGTAACCA GGTCCAATCA 960  
 GTAAAAATAA GCTGCTTATA A 981

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 984 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..984
  - (D) OTHER INFORMATION: /note= "(OCIF-DDD2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATGAACAACACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60  
 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120  
 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180  
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240  
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300  
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360  
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCAGAG GCGAAATACA 420  
 GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT 480  
 AGAAAACACA CAAATTGCAG TGTCTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540  
 CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC 600

CTGTGTGAGG AGGCATT CAGGTTTGCT GTTCCTACAA AGTTTAC TAACTGGCTT 660  
 AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720  
 AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780  
 AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGACG CACTAAAGCA CTCAAAGACG 840  
 TACCACTTTC CAAAACCTGT CACTCAGAGT CTAAAGAAGA CCATCAGGTT CCTTCACAGC 900  
 TTCACAATGT ACAAATTGTA TCAGAAGTTA TTTTATAGAA TGATAGGTAA CCAGGTCCAA 960  
 TCAGTAAAAA TAAGCTGCTT ATAA 984

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1200 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: -  
 (B) LOCATION: 1..1200  
 (D) OTHER INFORMATION: /note= "(OCIF-CL)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60  
 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120  
 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180  
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240  
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300  
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360  
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCAGA GCGAAATACA 420  
 GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT 480  
 AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540  
 CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC 600  
 CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT 660  
 AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720  
 AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780  
 AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC 840  
 GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900  
 AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA 960  
 CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC 1020

[illegible]

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1056 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

(2) INFORMATION FOR SEQ ID NO:96:

## 64



[illegible]

(ix) **FEATURE:**

(B) LOCATION: 1..819

(D) OTHER INFORMATION: /note= "(OCIF-CDD2)"

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| ATGAACAACCT | TGCTGTGCTG | CGCGCTCGTG | TTTCTGGACA | TCTCCATTAA | GTGGACCACC  | 60  |
| CAGGAAACGT  | TTCCTCCAAA | GTACCTTCAT | TATGACGAAG | AAACCTCTCA | TCAGCTGTTG  | 120 |
| TGTGACAAAT  | GTCCTCCTGG | TACCTACCTA | AAACAACACT | GTACAGCAAA | GTGGAAGACC  | 180 |
| GTGTGCGCCC  | CTTGCCCTGA | CCACTACTAC | ACAGACAGCT | GGCACACCAG | TGACGAGTGT  | 240 |
| CTATACTGCA  | GCCCCGTGTG | CAAGGAGCTG | CAGTACGTCA | AGCAGGAGTG | CAATCGCACC  | 300 |
| CACAACCGCG  | TGTGCGAATG | CAAGGAAGGG | CGCTACCTTG | AGATAGAGTT | CTGCTTGAAA  | 360 |
| CATAGGAGCT  | GCCCTCCTGG | ATTTGGAGTG | GTGCAAGCTG | GAACCCCA   | GCGAAATACA  | 420 |
| GTTTGCAAAA  | GATGTCCAGA | TGGGTTCCTC | TCAAATGAGA | CGTCATCTAA | AGCACCCCTGT | 480 |
| AGAAAACACA  | CAAATTGCAG | TGTCTTTGGT | CTCCTGCTAA | CTCAGAAAGG | AAATGCAACA  | 540 |
| CACGACAACA  | TATGTTCCGG | AAACAGTGAA | TCAACTCAAA | AATGTGGAAT | AGATGTTACC  | 600 |
| CTGTGTGAGG  | AGGCATTCTT | CAGGTTTGCT | GTTCTTACAA | AGTTTACGCC | TAACTGGCTT  | 660 |
| AGTGTTCTTG  | TAGACAATTT | GCCTGGCACC | AAAGTAAACG | CAGAGAGTGT | AGAGAGGATA  | 720 |
| AAACGGCAAC  | ACAGCTCACA | AGAACAGACT | TTCCAGCTGC | TGAAGTTATG | GAAACATCAA  | 780 |
| AAACAAAGACC | AAGATATAGT | CAAGAAGATC | ATCCAATGA  |            |             | 819 |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 594 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..594

(D) OTHER INFORMATION: /note= "(OCIF-CDD1)"

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ATGAACAAC  | TGCTGTGCTG | CGCGCTCGTG | TTTCTGGACA | TCTCCATTAA | GTGGACCACC | 60  |
| CAGGAAACGT | TTCCTCCAAA | GTACCTTCAT | TATGACGAAG | AAACCTCTCA | TCAGCTGTTG | 120 |
| TGTGACAAAT | GTCCTCCTGG | TACCTACCTA | AAACAACACT | GTACAGCAAA | GTGGAAGACC | 180 |
| GTGTGCGCCC | CTTGCCCTGA | CCACTACTAC | ACAGACAGCT | GGCACACCAG | TGACGAGTGT | 240 |

CTATACTGCA GCCCCTGCA CAAGGAGCTG CAGTACGTCA AGCAGGAGT CAATCGCACC 300  
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360  
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAAGA GCGAAATACA 420  
 GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT 480  
 AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540  
 CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT ATGA 594

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 432 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: -  
 (B) LOCATION: 1..432  
 (D) OTHER INFORMATION: /note= "(OCIF-CCR4)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60  
 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120  
 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180  
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240  
 CTATACTGCA GCGCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300  
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360  
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAAGA GCGAAATACA 420  
 GTTTGCAAAAT GA 432

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 321 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: -  
 (B) LOCATION: 1..321  
 (D) OTHER INFORMATION: /note= "(OCIF-CCR3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60

|            |            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|------------|-----|
| CAGGAAACGT | TTC        | AA         | GTACCTTCAT | TATGACGAAG | AAACCTC    | TCAGCTGTTG | 120 |
| TGTGACAAAT | GTCCTCCTGG | TACCTACCTA | AAACAACACT | GTACAGCATA | GTGGAAGACC |            | 180 |
| GTGTGCGCCC | CTTGCCCTGA | CCACTACTAC | ACAGACAGCT | GGCACACCAG | TGACGAGTGT |            | 240 |
| CTATACTGCA | GCCCCGTGTG | CAAGGAGCTG | CAGTACGTCA | AGCAGGAGTG | CAATCGCACC |            | 300 |
| CACAACCGCG | TGTGCGAATG | A          |            |            |            |            | 321 |

(2) INFORMATION FOR SEQ ID NO:100:

(ii) MOLECULE TYPE: cDNA

- (A) NAME/KEY: -  
(B) LOCATION: 1..1182  
(D) OTHER INFORMATION: /note= "(OCIF-CBst)"

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 966 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..966  
(D) OTHER INFORMATION: /note= "(OCIF-CSph)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60  
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120  
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180  
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240  
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300  
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360  
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAAG GCGAAATACA 420  
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT 480  
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540  
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC 600  
CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT 660  
AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720  
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780  
AACAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAACAGC 840  
GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900  
AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCTAGTCTA 960  
GACTAG 966

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 564 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC | 60  |
| CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG | 120 |
| TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC | 180 |
| GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT | 240 |
| CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC | 300 |
| CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA | 360 |
| CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCAGA GCGAAATACA  | 420 |
| GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT  | 480 |
| AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA | 540 |
| CACGACAACA TATGTTCCGG CTAG                                        | 564 |

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 255 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..255
- (D) OTHER INFORMATION: /note= "(OCIF-Pst)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC | 60  |
| CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG | 120 |
| TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC | 180 |
| GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT | 240 |
| CTATACCTAG TCTAG                                                  | 255 |

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1317 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1317

(D) OTHER INFORMATION: /note= "human OC10 genomic DNA-1"

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 1173..1202

(D) OTHER INFORMATION: /note= "amino acid residues -21 to -12"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CTGGAGACAT ATAACCTGAA CACTTGGCCC TGATGGGGAA GCAGCTCTGC AGGGACTTTT 60  
TCAGCCATCT GTAAACAATT TCAGTGGCAA CCCGCGAACT GTAATCCATG AATGGGACCA 120  
CACTTTACAA GTCATCAAGT CTAACCTCTA GACCAGGGAA TTAATGGGGG AGACAGCGAA 180  
CCCTAGAGCA AAGTGCCAAA CTTCTGTCTG TAGCTTGAGG CTAGTGAAA GACCTCGAGG 240  
AGGCTACTCC AGAAGTTCAG CGCGTAGGAA GCTCCGATAC CAATAGCCCT TTGATGATGG 300  
TGGGGTTGGT GAAGGGAACA GTGCTCCGCA AGGTTATCCC TGCCCCAGGC AGTCCAATTT 360  
TCACTCTGCA GATTCTCTCT GGCTCTAACT ACCCCAGATA ACAAGGAGTG AATGCAGAAT 420  
AGCACGGGCT TTAGGGCCAA TCAGACATTA GTTAGAAAAA TTCCTACTAC ATGGTTTATG 480  
TAAACTTGAA GATGAATGAT TGCGAACCTC CCGAAAAGGG CTCAGACAAT GCCATGCATA 540  
AAGAGGGGCC CTGTAATTTG AGGTTTCAGA ACCCGAAGTG AAGGGGTCAG GCAGCCGGGT 600  
ACGGCGGAAA CTCACAGCTT TCGCCAGCG AGAGGACAAA GGCTCTGGGAC AACTCCAAC 660  
TGCGTCCGGA TCTTGCTGAG ATCGGACTCT CAGGGTGGAG GAGACACAAG CACAGCAGCT 720  
GCCCAGCGTG TGCCAGCCC TCCACCGCT GGTCCTGGCT GCCAGGAGGC TGGCCGCTGG 780  
CGGGAAGGGG CCGGAAACC TCAGAGCCCC GCGGAGACAG CAGCCGCCTT GTTCCTCAGC 840  
CCGGTGGCTT TTTTTCCTCC TGCTCTCCA GGGGACAGAC ACCACCGCCC CACCCCTCAC 900  
GCCCCACCTC CCTGGGGGAT CCTTTCGCC CCAGCCCTGA AAGCGTTAAT CCTGGAGCTT 960  
TCTGCACACC CCCCAGCCGC TCCCGCCCAA GCTTCTAAA AAAGAAAGGT GCAAAGTTTG 1020  
GTCCAGGATA GAAAAATGAC TGATCAAAGG CAGGCGATAC TTCCTGTTGC CGGGACGCTA 1080  
TATATAACGT GATGAGCGCA CGGGCTGCGG AGACGCACCG GAGCGCTCGC CCAGCCGCCG 1140  
CCTCCAAGCC CTGAGGTTT CCGGGGACCA CAATGAACAA GTTGCTGTGC TGCGCGCTCG 1200  
TGGTAAGTCC CTGGGCCAGC CGACGGGTGC CCGGCGCTG GGGAGGCTGC TGCCACCTGG 1260  
TCTCCAACC TCCAGCGGA CCGCGGGGA AAAAGGCTCC ACTCGCTCCC TCCAAG 1317

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10190 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 130..162

```
(A) NAME/KEY: CDS
(B) LOCATION: join(130..162, 163..498, 4503..4694, 6715..6939,
 8960..9346)
```

```
(A) NAME/KEY: mat_peptide
(B) LOCATION: join(163..498, 4503..4694, 6715..6939, 8960..9346)
```

|                                                                 |                                                     |            |            |            |            |     |      |
|-----------------------------------------------------------------|-----------------------------------------------------|------------|------------|------------|------------|-----|------|
| GCTTACTTTTG                                                     | ATGCAAAATCT                                         | CATTAGGCTT | AAGGTAATAC | AGGACTTTGA | GTCAAATGAT |     | 60   |
| ACTGTTGCAC                                                      | ATAAGAACAA                                          | ACCTATTTTC | ATGCTAAGAT | GATGCCACTG | TGTTCTTTTC |     | 120  |
| TCCTTCTAG                                                       | TTT CTG GAC ATC TCC ATT AAG TGG ACC ACC CAG GAA ACG |            |            |            |            |     | 168  |
|                                                                 | Phe Leu Asp Ile Ser Ile Lys Trp Thr Thr Gln Glu Thr |            |            |            |            |     |      |
|                                                                 | -11 -10                                             |            | -5         |            | 1          |     |      |
| TTT CCT CCA AAG TAC CTT CAT TAT GAC GAA GAA ACC TCT CAT CAG CTG |                                                     |            |            |            |            |     | 216  |
| Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His Gln Leu |                                                     |            |            |            |            |     |      |
|                                                                 | 5                                                   |            | 10         |            | 15         |     |      |
| TTG TGT GAC AAA TGT CCT CCT GGT ACC TAC CTA AAA CAA CAC TGT ACA |                                                     |            |            |            |            |     | 264  |
| Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His Cys Thr |                                                     |            |            |            |            |     |      |
|                                                                 | 20                                                  |            | 25         |            | 30         |     |      |
| GCA AAG TGG AAG ACC GTG TGC GCC CCT TGC CCT GAC CAC TAC TAC ACA |                                                     |            |            |            |            |     | 312  |
| Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr |                                                     |            |            |            |            |     |      |
|                                                                 | 35                                                  |            | 40         |            | 45         |     | 50   |
| GAC AGC TGG CAC ACC AGT GAC GAG TGT CTA TAC TGC AGC CCC GTG TGC |                                                     |            |            |            |            |     | 360  |
| Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys |                                                     |            |            |            |            |     |      |
|                                                                 |                                                     | 55         |            |            | 60         |     | 65   |
| AAG GAG CTG CAG TAC GTC AAG CAG GAG TGC AAT CGC ACC CAC AAC CGC |                                                     |            |            |            |            |     | 408  |
| Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg |                                                     |            |            |            |            |     |      |
|                                                                 |                                                     | 70         |            |            | 75         |     | 80   |
| GTG TGC GAA TGC AAG GAA GGG CGC TAC CTT GAG ATA GAG TTC TGC TTG |                                                     |            |            |            |            |     | 456  |
| Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu |                                                     |            |            |            |            |     |      |
|                                                                 |                                                     | 85         |            |            | 90         |     | 95   |
| AAA CAT AGG AGC TGC CCT CCT GGA TTT GGA GTG GTG CAA GCT         |                                                     |            |            |            |            |     | 498  |
| Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala         |                                                     |            |            |            |            |     |      |
|                                                                 | 100                                                 |            |            | 105        |            | 110 |      |
| GGTACGTGTC                                                      | AATGTGCAGC                                          | AAAATTAATT | AGGATCATGC | AAAGTCAGAT | AGTTGTGACA |     | 558  |
| GTTTAGGAGA                                                      | ACACTTTTGT                                          | TCTGATGACA | TTATAGGATA | GCAAATTGCA | AAGGTAATGA |     | 618  |
| AACCTGCCAG                                                      | GTAGGTACTA                                          | TGTGTCTGGA | GTGCTTCCAA | AGGACCATTG | CTCAGAGGAA |     | 678  |
| TACTTTGCCA                                                      | CTACAGGGCA                                          | ATTTAATGAC | AAATCTCAAA | TGCAGCAAAT | TATTCTCTCA |     | 738  |
| TGAGATGCAT                                                      | GATGGTTTTT                                          | TTTTTTTTTT | TTAAAGAAAC | AAACTCAAGT | TGCACTATTG |     | 798  |
| ATAGTTGATC                                                      | TATACCTCTA                                          | TATTTCACTT | CAGCATGGAC | ACCTTCAAAC | TGCAGCACTT |     | 858  |
| TTTGACAAAC                                                      | ATCAGAAATG                                          | TTAATTTATA | CCAAGAGAGT | AATTATGCTC | ATATTAATGA |     | 918  |
| GA CTCTGGAG                                                     | TGCTAACAAT                                          | AAGCAGTTAT | AATTAATTAT | GTAAAAAATG | AGAATGGTGA |     | 978  |
| GGGGAATTGC                                                      | ATTTCAATTAT                                         | TAAAAACAAG | GCTAGTTCTT | CCTTTAGCAT | GGGAGCTGAG |     | 1038 |

[illegible]





|            |            |             |                                 |            |             |      |
|------------|------------|-------------|---------------------------------|------------|-------------|------|
| GGCCTCCAGC | CACGTTTG   | GTCAAACCTTA | CATTTTCCTT                      | TTCTTGG    | TTAAACAGCT  | 4824 |
| AAGGCTACTC | TCGATGCATT | ACTGCTAAAG  | CTACCACTCA                      | GAATCTCTCA | AAAACCTCATC | 4884 |
| TTCTCACAGA | TAACACCTCA | AAGCTTGATT  | TTCTCTCCTT                      | TCACACTGAA | ATCAAATCTT  | 4944 |
| GCCCATAGGC | AAAGGGCAGT | GTCAAGTTTG  | CCACTGAGAT                      | GAAATTAGGA | GAGTCCAAAC  | 5004 |
| TGTAGAATTC | ACGTTGTGTG | TTATTACTTT  | CACGAATGTC                      | TGTATTATTA | ACTAAAGTAT  | 5064 |
| ATATTGGCAA | CTAAGAAGCA | AAGTGATATA  | AACATGATGA                      | CAAATTAGGC | CAGGCATGGT  | 5124 |
| GGCTTACTCC | TATAATCCCA | ACATTTTGGG  | GGGCCAAGGT                      | AGGCAGATCA | CTTGAGGTCA  | 5184 |
| GGATTTCAAG | ACCAGCCTGA | CCAACATGGT  | GAAACCTTGT                      | CTCTACTAAA | AATACAAAAA  | 5244 |
| TTAGCTGGGC | ATGGTAGCAG | GCACTTCTAG  | TACCAGCTAC                      | TCAGGGCTGA | GGCAGGAGAA  | 5304 |
| TCGCTTGAAC | CCAGGAGATG | GAGGTTGCAG  | TGAGCTGAGA                      | TTGTACCACT | GCACTCCAGT  | 5364 |
| CTGGGCAACA | GAGCAAGATT | TCATCACACA  | CACACACACA                      | CACACACACA | CACACATTAG  | 5424 |
| AAATGTGTAC | TTGGCTTTGT | TACCTATGGT  | ATTAGTGCAT                      | CTATTGCATG | GAACTTCCAA  | 5484 |
| GCTACTCTGG | TTGTGTTAAG | CTCTTCATTG  | GGTACAGGTC                      | ACTAGTATTA | AGTTCAGGTT  | 5544 |
| ATTCCGATGC | ATTCCACGGT | AGTGATGACA  | ATTCACTCAGG                     | CTAGTGTGTG | TGTTCCACCTT | 5604 |
| GTCACTCCCA | CCACTAGACT | AATCTCAGAC  | CTTCACTCAA                      | AGACACATTA | CACTAAAGAT  | 5664 |
| GATTTGCTTT | TTTGTGTTTA | ATCAAGCAAT  | GGTATAAACC                      | AGCTTGACTC | TCCCCAAACA  | 5724 |
| GTTTTTCGTA | CTACAAAGAA | GTTTATGAAG  | CAGAGAAATG                      | TGAATTGATA | TATATATGAG  | 5784 |
| ATTCTAACCC | AGTTCAGCA  | TTGTTTCATT  | GTGTAATTGA                      | AATCATAGAC | AAGCCATTTT  | 5844 |
| AGCCTTTGCT | TTCTTATCTA | AAAAAAAAAA  | AAAAAAAAATG                     | AAGGAAGGGG | TATTAAGG    | 5904 |
| AGTGATCAAA | TTTTAACATT | CTCTTTAATT  | AATTCATTTT                      | TAATTTTACT | TTTTTTCATT  | 5964 |
| TATTGTGCAC | TTACTATGTG | GTACTGTGCT  | ATAGAGGCTT                      | TAACATTTAT | AAAAACACTG  | 6024 |
| TGAAAGTTGC | TTCAGATGAA | TATAGGTAGT  | AGAACGGCAG                      | AACTAGTATT | CAAAGCCAGG  | 6084 |
| TCTGATGAAT | CCAAAAACAA | ACACCCATTA  | CTCCCATTTT                      | CTGGGACATA | CTTACTCTAC  | 6144 |
| CCAGATGCTC | TGGGCTTTGT | AATGCCTATG  | TAAATAACAT                      | AGTTTTATGT | TTGGTTATTT  | 6204 |
| TCCTATGTAA | TGTCTACTTA | TATATCTGTA  | TCTATCTCTT                      | GCTTTGTTTC | CAAAGGTAAA  | 6264 |
| CTATGTGTCT | AAATGTGGGC | AAAAAATAAC  | ACACTATTCC                      | AAATTACTGT | TCAAATTCCT  | 6324 |
| TTAAGTCAGT | GATAATTATT | TGTTTTGACA  | TTAATCATGA                      | AGTTCCCTGT | GGGTACTAGG  | 6384 |
| TAAACCTTTA | ATAGAATGTT | AATGTTTGTA  | TTCATTATAA                      | GAATTTTTGG | CTGTTACTTA  | 6444 |
| TTTACAACAA | TATTTCACTC | TAATTAGACA  | TTTACTAAAC                      | TTTCTCTTGA | AAACAATGCC  | 6504 |
| CAAAAAAGAA | CATTAGAAGA | CACGTAAGCT  | CAGTTGGTCT                      | CTGCCACTAA | GACCAGCCAA  | 6564 |
| CAGAAGCTTG | ATTTTATTCA | AACTTTGCAT  | TTTAGCATAT                      | TTTATCTTGG | AAAATTCAAT  | 6624 |
| TGTGTTGGTT | TTTTGTTTTT | GTTTGTATTG  | AATAGACTCT                      | CAGAAATCCA | ATTGTTGAGT  | 6684 |
| AAATCTTCTG | GGTTTTCTAA | CCTTCTTTA   | GAT GTT ACC CTG TGT GAG GAG GCA |            |             | 6738 |
|            |            |             | Asp Val Thr Leu Cys Glu Glu Ala |            |             |      |
|            |            |             | 180                             |            |             |      |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| TTC TTC AGG TTT TTT GAT CCT ACA AAG TTT ACG CCT AAC TTT CTT AGT    | 6786 |
| Phe Phe Arg Phe Val Pro Thr Lys Phe Thr Pro Asn Leu Ser            |      |
| 185 190 195 200                                                    |      |
| GTC TTG GTA GAC AAT TTG CCT GGC ACC AAA GTA AAC GCA GAG AGT GTA    | 6834 |
| Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val    |      |
| 205 210 215                                                        |      |
| GAG AGG ATA AAA CGG CAA CAC AGC TCA CAA GAA CAG ACT TTC CAG CTG    | 6882 |
| Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu    |      |
| 220 225 230                                                        |      |
| CTG AAG TTA TGG AAA CAT CAA AAC AAA GAC CAA GAT ATA GTC AAG AAG    | 6930 |
| Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys    |      |
| 235 240 245                                                        |      |
| ATC ATC CAA GGTAATTACA TTCCAAAATA CGTCTTTGTA CGATTTTGTG            | 6979 |
| Ile Ile Gln                                                        |      |
| 250                                                                |      |
| GTATCATCTC TCTCTCTGAG TTGAACACAA GGCCTCCAGC CACATTCTTG GTCAAACCTTA | 7039 |
| CATTTTCCCT TTCTTGAATC TTAACCAGCT AAGGCTACTC TCGATGCATT ACTGCTAAAG  | 7099 |
| CTACCACTCA GAATCTCTCA AAAACTCATC TTCTCACAGA TAACACCTCA AAGCTTGATT  | 7159 |
| TTCTCTCCTT TCACACTGAA ATCAAATCTT GCCCATAGGC AAAGGGCAGT GTCAAGTTTG  | 7219 |
| CCACTGAGAT GAAATTAGGA GAGTCCAAAC TGTAGAATTC ACGTTGTGTG TTATTACTTT  | 7279 |
| CACGAATGTC TGTATTATTA ACTAAAGTAT ATATTGGCAA CTAAGAAGCA AAGTGATATA  | 7339 |
| AACATGATGA CAAATTAGGC CAGGCATGGT GGCTTACTCC TATAATCCCA ACATTTTGGG  | 7399 |
| GGGCCAAGGT AGGCAGATCA CTTGAGGTCA GGATTTC AAG ACCAGCCTGA CCAACATGGT | 7459 |
| GAAACCTTGT CTCTACTAAA AATACAAAAA TTAGCTGGGC ATGGTAGCAG GCACTTCTAG  | 7519 |
| TACCAGCTAC TCAGGGCTGA GGCAGGAGAA TCGCTTGAAC CCAGGAGATG GAGGTTGCAG  | 7579 |
| TGAGCTGAGA TTGTACCACT GCACTCCAGT CTGGGCAACA GAGCAAGATT TCATCACACA  | 7639 |
| CACACACACA CACACACACA CACACATTAG AAATGTGTAC TTGGCTTTGT TACCTATGGT  | 7699 |
| ATTAGTGCAT CTATTGCATG GAACTTCCAA GCTACTCTGG TTGTGTTAAG CTCTTCATTG  | 7759 |
| GGTACAGGTC ACTAGTATTA AGTTCAGGTT ATTCCGATGC ATTCCACGGT AGTGATGACA  | 7819 |
| ATTCATCAGG CTAGTGTGTG TGTTACCTT GTCCTCCCA CCACTAGACT AATCTCAGAC    | 7879 |
| CTTCACTCAA AGACACATTA CACTAAAGAT GATTTGCTTT TTTGTGTTTA ATCAAGCAAT  | 7939 |
| GGTATAAACC AGCTTGACTC TCCCCAAACA GTTTTTCGTA CTACAAAGAA GTTTATGAAG  | 7999 |
| CAGAGAAATG TGAATTGATA TATATATGAG ATTCTAACCC AGTTCCAGCA TTGTTTCATT  | 8059 |
| GTGTAATTGA AATCATAGAC AAGCCATTTT AGCCTTTGCT TTCTTATCTA AAAAAAAAAA  | 8119 |
| AAAAAAAAATG AAGGAAGGGG TATTAAAAGG AGTGATCAAA TTTTAACATT CTCTTTAATT | 8179 |
| AATTCATTTT TAATTTTACT TTTTTCATT TATTGTGCAC TTACTATGTG GTACTGTGCT   | 8239 |
| ATAGAGGCTT TAACATTTAT AAAAACA CTG TGAAAGTTGC TTCAGATGAA TATAGGTAGT | 8299 |
| AGAACGGCAG AACTAGTATT CAAAGCCAGG TCTGATGAAT CCAAAAACAA ACACCCATTA  | 8359 |
| CTCCCATTTT CTGGGACATA CTTACTCTAC CCAGATGCTC TGGGCTTTGT AATGCCTATG  | 8419 |



ATCCTATAAA GAAATAT GACTTAATTT TAGAAAGAAA ATTATAT GTTTATTATG 9876  
 ACAAATGAAA GAGAAATAT ATATTTTAA TGGAAAGTTT GTAGCAT TCTAATAGGT 9936  
 ACTGCCATAT TTTTCTGTGT GGAGTATTTT TATAATTTTA TCTGTATAAG CTGTAATATC 9996  
 ATTTTATAGA AAATGCATTA TTTAGTCAAT TGTTTAATGT TGGAAAACAT ATGAAATATA 10056  
 AATTATCTGA ATATTAGATG CTCTGAGAAA TTGAATGTAC CTTATTTAAA AGATTTTATG 10116  
 GTTTTATAAC TATATAAATG ACATTATTAA AGTTTTCAAA TTATTTTITA TTGCTTTCTC 10176  
 TGTGCTTTT ATTT 10190

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 391 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Phe Leu Asp Ile Ser Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro  
 -11 -10 -5 1 5  
 Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp  
 10 15 20  
 Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp  
 25 30 35  
 Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp  
 40 45 50  
 His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu  
 55 60 65  
 Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys Glu  
 70 75 80 85  
 Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys His Arg  
 90 95 100  
 Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr Pro Glu Arg  
 105 110 115  
 Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr  
 120 125 130  
 Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser Val Phe Gly  
 135 140 145  
 Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn Ile Cys Ser  
 150 155 160 165  
 Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val Thr Leu Cys  
 170 175 180  
 Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe Thr Pro Asn  
 185 190 195  
 Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn Ala  
 200 205 210

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----|
| Glu<br>215 | Ser        | Val        | Glu        | Arg<br>216 | Lys        | Arg        | Gln        | His        | Ser        | Ser<br>225 | Gln        | Ala        | Gln        | Thr |
| Phe<br>230 | Gln        | Leu        | Leu        | Lys        | Leu<br>235 | Trp        | Lys        | His        | Gln        | Asn<br>240 | Lys        | Asp        | Gln        | Asp |
| Val        | Lys        | Lys        | Ile        | Ile<br>250 | Gln        | Asp        | Ile        | Asp        | Leu<br>255 | Cys        | Glu        | Asn        | Ser        | Val |
| Arg        | His        | Ile        | Gly<br>265 | His        | Ala        | Asn        | Leu        | Thr<br>270 | Phe        | Glu        | Gln        | Leu        | Arg<br>275 | Ser |
| Met        | Glu        | Ser<br>280 | Leu        | Pro        | Gly        | Lys        | Lys<br>285 | Val        | Gly        | Ala        | Glu        | Asp<br>290 | Ile        | Glu |
| Thr        | Ile<br>295 | Lys        | Ala        | Cys        | Lys        | Pro<br>300 | Ser        | Asp        | Gln        | Ile        | Leu<br>305 | Lys        | Leu        | Ser |
| Leu<br>310 | Trp        | Arg        | Ile        | Lys        | Asn<br>315 | Gly        | Asp        | Gln        | Asp        | Thr<br>320 | Leu        | Lys        | Gly        | Leu |
| His        | Ala        | Leu        | Lys        | His<br>330 | Ser        | Lys        | Thr        | Tyr        | His<br>335 | Phe        | Pro        | Lys        | Thr<br>340 | Val |
| Gln        | Ser        | Leu        | Lys<br>345 | Lys        | Thr        | Ile        | Arg        | Phe<br>350 | Leu        | His        | Ser        | Phe        | Thr<br>355 | Met |
| Lys        | Leu        | Tyr<br>360 | Gln        | Lys        | Leu        | Phe<br>365 | Leu        | Glu        | Met        | Ile        | Gly        | Asn<br>370 | Gln        | Val |
| Ser<br>375 | Val        | Lys        | Ile        | Ser        | Cys<br>380 | Leu        |            |            |            |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:107:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (A) NAME/KEY: -  
(B) LOCATION: 1..21  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer 3R)"

YTTRTACATN GTRAANSWRT G

**SECRET**